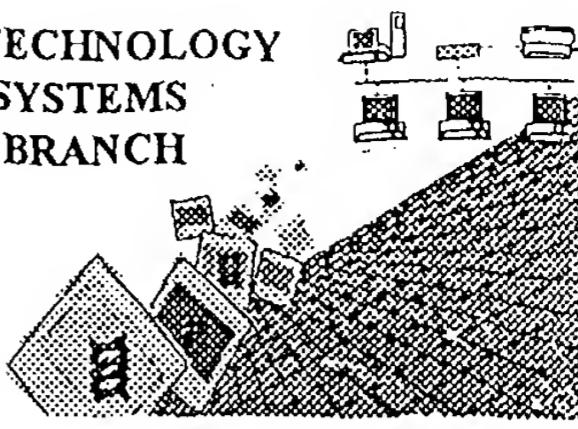


BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/647,732
Source: 1 Fwd -
Date Processed by STIC: 12/22/03 ~

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

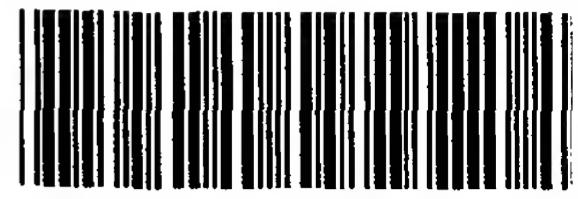
SUGGESTED CORRECTION

SERIAL NUMBER: 10/647,732

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- | | | |
|----|------------------------------------|--|
| 1 | Wrapped Nucleic
Wrapped Aminos | The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping." |
| 2 | Invalid Line Length | The rules require that a line not exceed 72 characters in length. This includes white spaces. |
| 3 | Misaligned Amino
Numbering | The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead. |
| 4 | Non-ASCII | The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text. |
| 5 | Variable Length | Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing. |
| 6 | PatentIn 2.0
"bug" | A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences. |
| 7 | Skipped Sequences
(OLD RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences. |
| 8 | Skipped Sequences
(NEW RULES) | Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000 |
| 9 | Use of n's or Xaa's
(NEW RULES) | Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents. |
| 10 | Invalid <213>
Response | Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence |
| 11 | Use of <220> | Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules) |
| 12 | PatentIn 2.0
"bug" | Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk. |
| 13 | Misuse of n/Xaa | "n" can only represent a single <u>nucleotide</u> ; "Xaa" can only represent a single <u>amino acid</u> |



RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/647,732

DATE: 12/22/2003

TIME: 15:34:19

Input Set : A:\PTO.LN.txt
 Output Set: N:\CRF4\12222003\J647732.raw

IMPORTANT: see item 4 on
Error Summary
Sheet

4 <110> APPLICANT: The University of Connecticut
 5 Chen, Thomas
 6 Chen, Maria
 8 <120> TITLE OF INVENTION: Antitumor Activity of Ea-2 and Ea-4 Peptide of Pro-IGF-1
 10 <130> FILE REFERENCE: UCT97-044
 12 <140> CURRENT APPLICATION NUMBER: US 10/647,732
 13 <141> CURRENT FILING DATE: 2003-08-25
 15 <150> PRIOR APPLICATION NUMBER: 09/669,642
 16 <151> PRIOR FILING DATE: 2000-09-26
 18 <160> NUMBER OF SEQ ID NOS: 6
 20 <170> SOFTWARE: PatentIn version 3.0

ORED SEQUENCES

22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 35
 24 <212> TYPE: PRT
 25 <213> ORGANISM: Onchorhynchus mykiss
 28 <400> SEQUENCE: 1
 30 Arg Ser Val Arg Ala Gln Arg His Thr Asp Met Pro Arg Thr Pro Lys
 > 31 1 5 10 15 → 20
 > 32 15 20 25
 34 Glu Val His Gln Lys Asn Ser Ser Arg Gly Asn Thr Gly Gly Arg Asn
 > 35 20 25
 > 36 30
 38 Tyr Arg Met
 > 39 35
 41 <210> SEQ ID NO: 2
 42 <211> LENGTH: 47
 43 <212> TYPE: PRT
 44 <213> ORGANISM: Oncorhynchus mykiss
 47 <400> SEQUENCE: 2
 51 Arg Ser Val Arg Ala Gln Arg His Thr Asp Met Pro Arg Thr Pro Lys
 > 52 1 5 10
 > 53 15
 55 Lys Pro Leu Ser Gly Asn Ser His Thr Ser Cys Lys Glu Val His Gln
 > 56 20 25
 > 57 30
 59 Lys Asn Ser Ser Arg Gly Asn Thr Gly Gly Arg Asn Tyr Arg Met
 > 60 35 40
 > 61 45
 63 <210> SEQ ID NO: 3

Does Not Comply
 Correct Dicrette Needed

see pp1-2

2) insert hard page
 breaks
 (see 1.824 of
 Sequence Rules)

see item 1 on
 Error Summary Sheet,
 also, see item 3 on
 Error Summary Sheet

same error

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/647,732

DATE: 12/22/2003
TIME: 15:34:19

Input Set : A:\PTO.LN.txt
Output Set: N:\CRF4\12222003\J647732.raw

```

64 <211> LENGTH: 62
65 <212> TYPE: PRT
66 <213> ORGANISM: Oncorhynchus mykiss
69 <400> SEQUENCE: 3
71 Arg Ser Val Arg Ala Gln Arg His Thr Asp Met Pro Arg Thr Pro Lys
> 72 1 5 10
> 73 15
75 Val Ser Thr Ala Val Gln Ser Val Asp Arg Gly Thr Glu Arg Arg Thr
> 76 20 25
> 77 30
79 Ala Gln His Pro Asp Lys Thr Lys Pro Lys Lys Glu Val His Gln Lys
> 80 35 40
> 81 45
83 Asn Ser Ser Arg Gly Asn Thr Gly Gly Arg Asn Tyr Arg Met
> 84 50 55 60
87 <210> SEQ ID NO: 4
88 <211> LENGTH: 74
89 <212> TYPE: PRT
90 <213> ORGANISM: Oncorhynchus mykiss
93 <400> SEQUENCE: 4
95 Arg Ser Val Arg Ala Gln Arg His Thr Asp Met Pro Arg Thr Pro Lys
> 96 1 5 10
> 97 15
99 Val Ser Thr Ala Val Gln Asn Val Asp Arg Gly Thr Glu Arg Arg Thr
> 100 20 25
> 101 30
102 Ala Gln His Pro Asp Lys Thr Lys Thr Lys Lys Pro Leu Ser Gly
> 103 35 40
> 104 45
109 Asn Ser His Thr Ser Cys Lys Glu Val His Gln Lys Asn Ser Ser Arg
> 110 50 55 60
112 Gly Asn Thr Gly Gly Arg Asn Tyr Arg Met
> 113 65 70
130 <210> SEQ ID NO: 6
131 <211> LENGTH: 30
132 <212> TYPE: DNA
133 <213> ORGANISM: Artificial Sequence
136 <220> FEATURE:
137 <221> NAME/KEY: misc_feature
138 <223> OTHER INFORMATION: derived from Oncorhynchus mykiss
141 <400> SEQUENCE: 6
142 ctccccgata tcctacattc ggttagttct 30
143 (30)? delete (same error in Sequence 5)
> 145 -19-of-26-
> 147 -20-of-26-
> 148 -21-of-26-

```

delete at end of file

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/647,732

DATE: 12/22/2003
TIME: 15:34:20

Input Set : A:\PTO.LN.txt
Output Set: N:\CRF4\12222003\J647732.raw

Valid Line Length:

rules require that a line not exceed 72 characters in length. This includes spaces.

#:1; Line(s) 31,35
#:2; Line(s) 52,56,60
#:3; Line(s) 72,76,84
#:4; Line(s) 96,100,110

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/647,732

DATE: 12/22/2003

TIME: 15:34:20

Input Set : A:\PTO.LN.txt

Output Set: N:\CRF4\12222003\J647732.raw

1 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
32 Repeated in SeqNo=1
2 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
32 Repeated in SeqNo=2
2 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
32 Repeated in SeqNo=3
6 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
32 Repeated in SeqNo=4
45 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:36 SEQ:6
45 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
54 Repeated in SeqNo=6
47 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
48 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:6
48 M:252 E: No. of Seq. differs, <211> LENGTH:Input:30 Found:48 SEQ:6